O.I.P.E
JUL 27 2006
PATENT & TRADEMARK OFFICE
IAP69

FIG. 1A

Range : 1 - 1053 Mode : Normal
Codon Table : Universal

```
            9          18          27          36          45          54
5'  ATG GGC GAC CCG GAA AGG CCG GAA GCG GCC GGG CTG GAT CAG GAT GAG AGA TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Gly Asp Pro Glu Arg Pro Glu Ala Ala Gly Leu Asp Gln Asp Glu Arg Ser

           63          72          81          90          99         108
    TCT TCA GAC ACC AAC GAA AGT GAA ATA AAG TCA AAT GAA GAG CCA CTC CTA AGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ser Ser Asp Thr Asn Glu Ser Glu Ile Lys Ser Asn Glu Glu Pro Leu Leu Arg

          117         126         135         144         153         162
    AAG AGT TCT CGC CGG TTT GTC ATC TTT CCA ATC CAG TAC CCT GAT ATT TGG AAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Lys Ser Ser Arg Arg Phe Val Ile Phe Pro Ile Gln Tyr Pro Asp Ile Trp Lys

          171         180         189         198         207         216
    ATG TAT AAA CAG GCA CAG GCT TCC TTC TGG ACA GCA GAA GAG GTC GAC TTA TCA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Tyr Lys Gln Ala Gln Ala Ser Phe Trp Thr Ala Glu Glu Val Asp Leu Ser

          225         234         243         252         261         270
    AAG GAT CTC CCT CAC TGG AAC AAG CTT AAA GCA GAT GAG AAG TAC TTC ATC TCT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Lys Asp Leu Pro His Trp Asn Lys Leu Lys Ala Asp Glu Lys Tyr Phe Ile Ser

          279         288         297         306         315         324
    CAC ATC TTA GCC TTT TTT GCA GCC AGT GAT GGA ATT GTA AAT GAA AAT TTG GTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    His Ile Leu Ala Phe Phe Ala Ala Ser Asp Gly Ile Val Asn Glu Asn Leu Val

          333         342         351         360         369         378
    GAG CGC TTT AGT CAG GAG GTG CAG GTT CCA GAG GCT CGC TGT TTC TAT GGC TTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Glu Arg Phe Ser Gln Glu Val Gln Val Pro Glu Ala Arg Cys Phe Tyr Gly Phe

          387         396         405         414         423         432
    CAA ATT CTC ATC GAG AAT GTT CAC TCA GAG ATG TAC AGT TTG CTG ATA GAC ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Gln Ile Leu Ile Glu Asn Val His Ser Glu Met Tyr Ser Leu Leu Ile Asp Thr
```

FIG. 1B

```
        441         450         459         468         477         486
TAC ATC AGA GAT CCC AAG AAA AGG GAA TTT TTA TTT AAT GCA ATT GAA ACC ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Tyr Ile Arg Asp Pro Lys Lys Arg Glu Phe Leu Phe Asn Ala Ile Glu Thr Met

        495         504         513         522         531         540
CCC TAT GTT AAG AAA AAA GCA GAT TGG GCC TTG CGA TGG ATA GCA GAT AGA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Pro Tyr Val Lys Lys Lys Ala Asp Trp Ala Leu Arg Trp Ile Ala Asp Arg Lys

        549         558         567         576         585         594
TCT ACT TTT GGG GAA AGA GTG GTG GCC TTT GCT GCT GTA GAA GGA GTT TTC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ser Thr Phe Gly Glu Arg Val Val Ala Phe Ala Ala Val Glu Gly Val Phe Phe
        603         612         621         630         639         648
TCA GGA TCT TTT GCT GCT ATA TTC TGG CTA AAG AAG AGA GGT CTT ATG CCA GGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ser Gly Ser Phe Ala Ala Ile Phe Trp Leu Lys Lys Arg Gly Leu Met Pro Gly

        657         666         675         684         693         702
CTC ACT TTT TCC AAT GAA CTC ATC AGC AGA GAT GAA GGA CTT CAC TGT GAC TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu His Cys Asp Phe

        711         720         729         738         747         756
GCT TGC CTG ATG TTC CAA TAC TTA GTA AAT AAG CCT TCA GAA GAA AGG GTC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Ala Cys Leu Met Phe Gln Tyr Leu Val Asn Lys Pro Ser Glu Glu Arg Val Arg

        765         774         783         792         801         810
GAG ATC ATT GTT GAT GCT GTC AAA ATT GAG CAG GAG TTT TTA ACA GAA GCC TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Glu Ile Ile Val Asp Ala Val Lys Ile Glu Gln Glu Phe Leu Thr Glu Ala Leu

        819         828         837         846         855         864
CCA GTT GGC CTC ATT GGA ATG AAT TGC ATT TTG ATG AAA CAG TAC ATT GAG TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Pro Val Gly Leu Ile Gly Met Asn Cys Ile Leu Met Lys Gln Tyr Ile Glu Phe

        873         882         891         900         909         918
GTA GCT GAC AGA TTA CTT GTG GAA CTT GGA TTC TCA AAG GTT TTT CAG GCA GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Ala Asp Arg Leu Leu Val Glu Leu Gly Phe Ser Lys Val Phe Gln Ala Glu
```

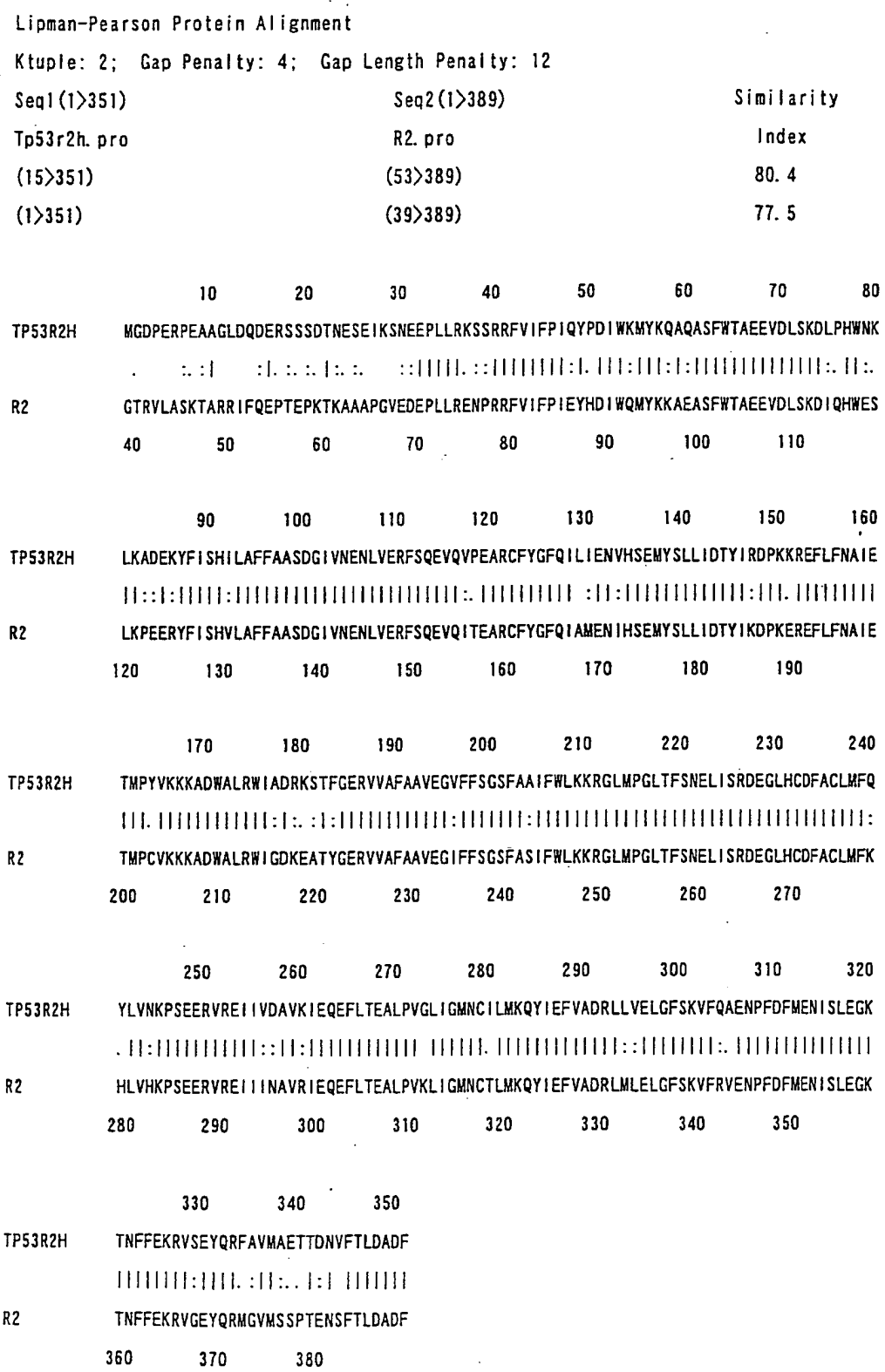
FIG. 1C

```
        927         936         945         954         963         972
AAT CCT TTT GAT TTT ATG GAA AAC ATT TCT TTA GAA GGA AAA ACA AAT TTC TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Asn Pro Phe Asp Phe Met Glu Asn Ile Ser Leu Glu Gly Lys Thr Asn Phe Phe

        981         990         999        1008        1017        1026
GAG AAA CGA GTT TCA GAG TAT CAG CGT TTT GCA GTT ATG GCA GAA ACC ACA GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Glu Lys Arg Val Ser Glu Tyr Gln Arg Phe Ala Val Met Ala Glu Thr Thr Asp

       1035        1044        1053
AAC GTC TTC ACC TTG GAT GCA GAT TTT 3'
--- --- --- --- --- --- --- --- ---
Asn Val Phe Thr Leu Asp Ala Asp Phe
```

FIG. 2


Lipman-Pearson Protein Alignment
Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12
Seq1(1>351)
Tp53r2h.pro
(15>351)
(1>351)
Seq2(1>389)
R2.pro
(53>389)
(39>389)
Similarity
Index
80.4
77.5
TP53R2H MGDPERPEAAGLDQDERSSSDTNESEIKSNEEPLLRKSSRRFVIFPIQYPDIWKMYKQAQASFWTAEEVDLSKDLPHWNK
R2 GTRVLASKTARRIFQEPTEPKTKAAAPGVEDEPLLRENPRRFVIFPIEYHDIWQMYKKAEASFWTAEEVDLSKDIQHWES
TP53R2H LKADEKYFISHILAFFAASDGIVNENLVERFSQEVQVPEARCFYGFQILIENVHSEMYSLLIDTYIRDPKKREFLFNAIE
R2 LKPEERYFISHVLAFFAASDGIVNENLVERFSQEVQITEARCFYGFQIAMENIHSEMYSLLIDTYIKDPKEREFLFNAIE
TP53R2H TMPYVKKKADWALRWIADRKSTFGERVVAFAAVEGVFFSGSFAAIFWLKKRGLMPGLTFSNELISRDEGLHCDFACLMFQ
R2 TMPCVKKKADWALRWIGDKEATYGERVVAFAAVEGIFFSGSFASIFWLKKRGLMPGLTFSNELISRDEGLHCDFACLMFK
TP53R2H YLVNKPSEERVREIIVDAVKIEQEFLTEALPVGLIGMNCILMKQYIEFVADRLLVELGFSKVFQAENPFDFMENISLEGK
R2 HLVHKPSEERVREIIINAVRIEQEFLTEALPVKLIGMNCTLMKQYIEFVADRLMLELGFSKVFRVENPFDFMENISLEGK
TP53R2H TNFFEKRVSEYQRFAVMAETTDNVFTLDADF
R2 TNFFEKRVGEYQRMGVMSSPTENSFTLDADF

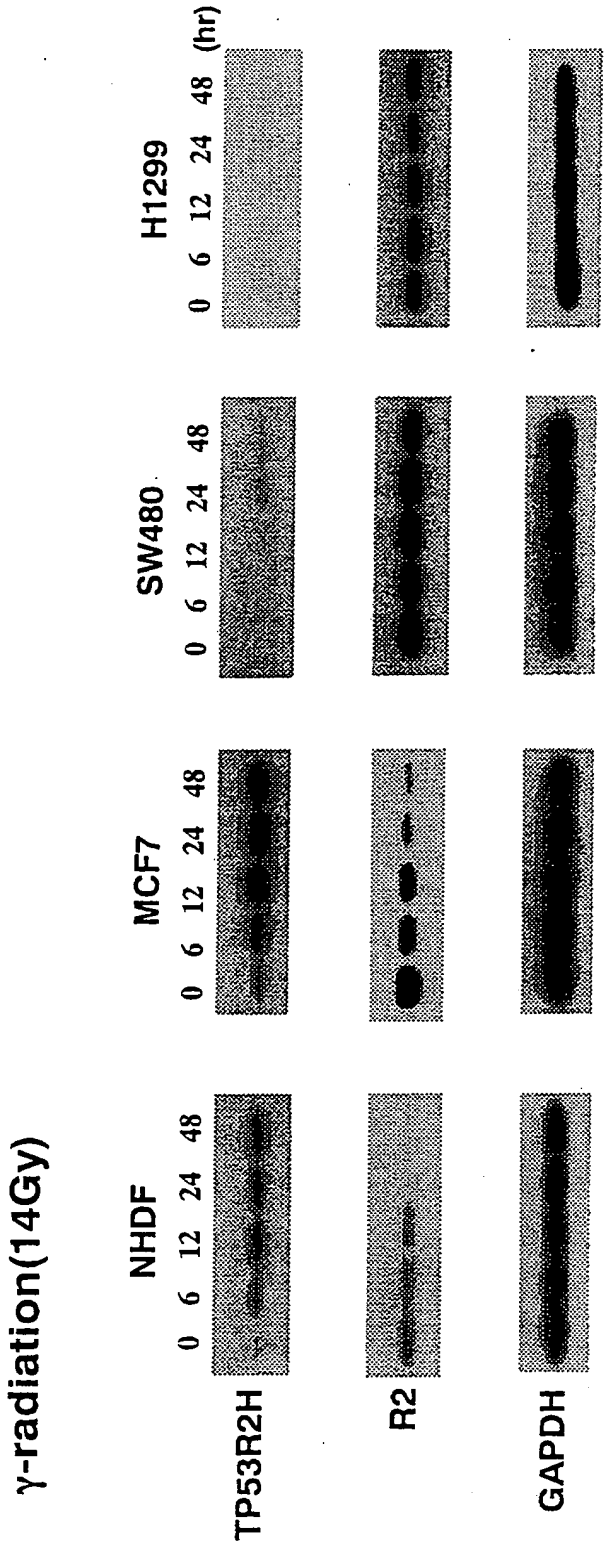

γ-radiation(14Gy)
NHDF
MCF7
SW480
H1299
0 6 12 24 48 (hr)
TP53R2H
R2
GAPDH

FIG. 3

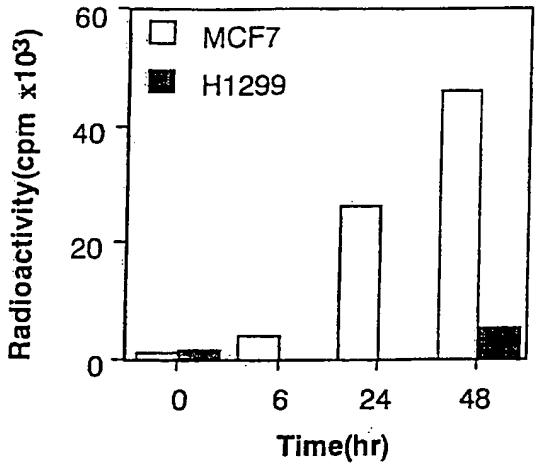

60
40
20
0
MCF7
H1299
Radioactivity(cpm x10³)
0
6
24
48
Time(hr)

FIG. 4

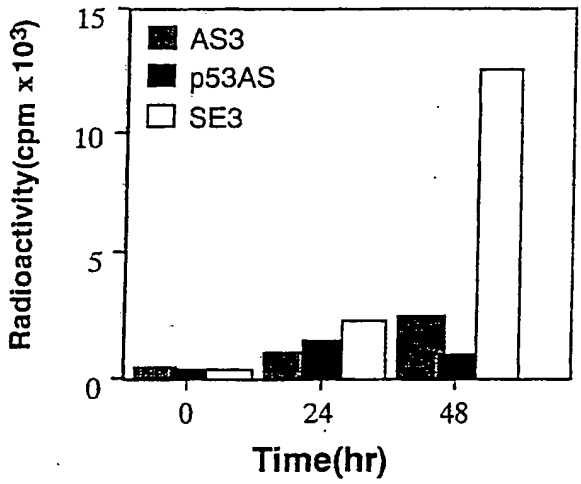

15
10
5
0
AS3
p53AS
SE3
Radioactivity(cpm x10³)
0
24
48
Time(hr)

FIG. 5

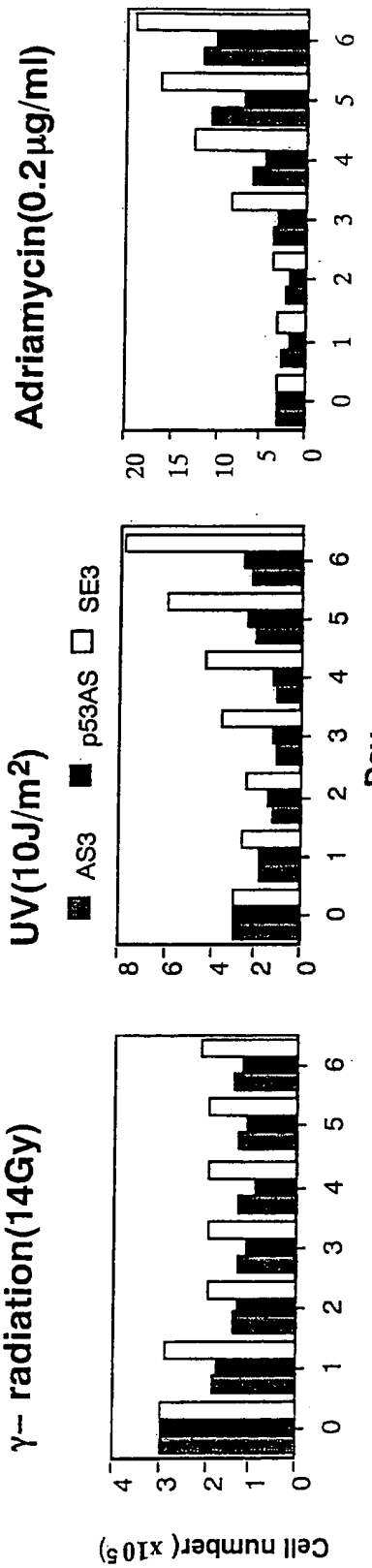


FIG. 6A

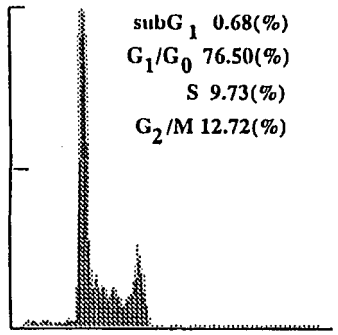
FIG. 6B

FIG. 6C

TP53R2H

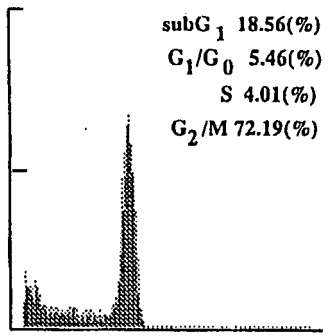
pcDNA3.1(+)

cells



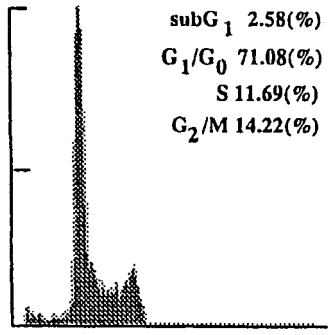
Adriamycin(0hr)

FIG. 7A



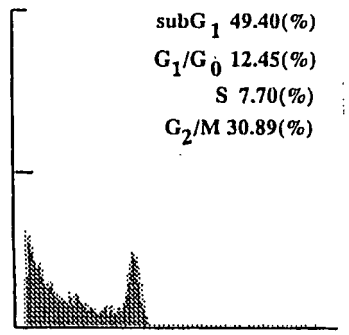
Adriamycin(48hr)

FIG. 7B



Adriamycin(0hr)

FIG. 7C



Adriamycin(48hr)

FIG. 7D